

SEQUENCE LISTING

<110> Yoshihiro OHMIYA, EMIKO ASHIDAKA and Seiji ITO

<120> Secreted or membrane-binding chimeric protein

<130> 200521/US

<160> 10

<170> PatentIn version 3.1

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<212> DNA

<213> Artificial Sequence

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<222> (1)..(2388)

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Leu Phe Asp Tyr Val Glu Thr Cys Ala Ala Pro Glu Thr Arg Gly Thr			
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tgt gtt tta tca gga cat act ttc tat gac aca ttc gac aaa gca aga			1008
Cys Val Leu Ser Gly His Thr Phe Tyr Asp Thr Phe Asp Lys Ala Arg			

325	330	335	
tat caa ttc cag ggc cca tgc aag gag att ctg atg gcc gca gac tgt			1056
Tyr Gln Phe Gln Gly Pro Cys Lys Glu Ile Leu Met Ala Ala Asp Cys			
340	345	350	
tac tgg aac aca tgg gat gta aag gtt tca cat aga gac gtc gaa tca			1104
Tyr Trp Asn Thr Trp Asp Val Lys Val Ser His Arg Asp Val Glu Ser			
355	360	365	
tac act gag gta gag aaa gta aca atc agg aaa cag tca act gta gta			1152
Tyr Thr Glu Val Glu Lys Val Thr Ile Arg Lys Gln Ser Thr Val Val			
370	375	380	
gat ctc att gtg gat ggc aag cag gtc aag gtt gga gga gtg gat gta			1200
Asp Leu Ile Val Asp Gly Lys Gln Val Lys Val Gly Gly Val Asp Val			
385	390	395	400
tct atc ccg tac agc tct gag aac act tcc ata tac tgg cag gat gga			1248
Ser Ile Pro Tyr Ser Ser Glu Asn Thr Ser Ile Tyr Trp Gln Asp Gly			
405	410	415	
gac atc ctg acg acg gcc atc cta cct gaa gct ctt gtc gtt aag ttc			1296
Asp Ile Leu Thr Thr Ala Ile Leu Pro Glu Ala Leu Val Val Lys Phe			
420	425	430	
aac ttt aag cag ctc ctt gta gtt cat atc aga gat cca ttc gat gga			1344
Asn Phe Lys Gln Leu Leu Val Val His Ile Arg Asp Pro Phe Asp Gly			
435	440	445	
aag aca tgc ggc ata tgt ggt aac tat aat caa gat tca act gat gat			1392
Lys Thr Cys Gly Ile Cys Gly Asn Tyr Asn Gln Asp Ser Thr Asp Asp			
450	455	460	
ttc ttt gac gca gaa gga gca tgc gct cta acc ccc aac ccc cca gga			1440
Phe Phe Asp Ala Glu Gly Ala Cys Ala Leu Thr Pro Asn Pro Pro Gly			

465	470	475	480	
tgt aca gag gaa cag aaa cca gaa gct gag cga ctt tgc aat aat ctc				1488
Cys Thr Glu Glu Gln Lys Pro Glu Ala Glu Arg Leu Cys Asn Asn Leu				
485	490	495		
ttt gat tct tct atc gac gag aaa tgt aat gtc tgc tac aag cct gac				1536
Phe Asp Ser Ser Ile Asp Glu Lys Cys Asn Val Cys Tyr Lys Pro Asp				
500	505	510		
cgg att gcc cga tgt atg tac gag tat tgc ctg agg gga caa caa gga				1584
Arg Ile Ala Arg Cys Met Tyr Glu Tyr Cys Leu Arg Gly Gln Gln Gly				
515	520	525		
ttt tgt gac cat gct tgg gag ttc aag aaa gaa tgc tac ata aaa cat				1632
Phe Cys Asp His Ala Trp Glu Phe Lys Lys Glu Cys Tyr Ile Lys His				
530	535	540		
gga gac act cta gaa gta cca cct gaa tgt caa gga tcc ctg gtt ggc				1680
Gly Asp Thr Leu Glu Val Pro Pro Glu Cys Gln Gly Ser Leu Val Gly				
545	550	555	560	
caa ctt ccg ggc cga ctt ccg ggc ccc ggt gaa gcc ccc gaa ccg ctt				1728
Gln Leu Pro Gly Arg Leu Pro Gly Pro Gly Glu Ala Pro Glu Pro Leu				
565	570	575		
ctg cag ctg ttt ctg ctc aat ctc ccc cac ctc ctc cag gcc ggg ctc				1776
Leu Gln Leu Phe Leu Leu Asn Leu Pro His Leu Leu Gln Ala Gly Leu				
580	585	590		
tgt gga tcc gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc				1824
Cys Gly Ser Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro				
595	600	605		
atc ctg gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg				1872
Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val				

610	615	620	
tcc ggc gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag			1920
Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys			
625	630	635	640
ttc atc tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg			1968
Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val			
645	650	655	
acc acc ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac			2016
Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His			
660	665	670	
atg aag cag cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc			2064
Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val			
675	680	685	
cag gag cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc			2112
Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg			
690	695	700	
gcc gag gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg			2160
Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu			
705	710	715	720
aag ggc atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg			2208
Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu			
725	730	735	
gag tac aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag			2256
Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln			
740	745	750	
aag aac ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac			2304
Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp			

755

760

765

ggc agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc 2352

Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly

770

775

780

gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc tac cag tcc 2400

Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser

785

790

795

800

gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg 2448

Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu

805

810

815

gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac 2496

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825

830

aag taa

2502

Lys

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Gln Leu Gln Lys Arg Phe Gly Gly Phe Thr Gly Ala Arg Lys Ser Ala

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30

Arg Lys Leu Ala Asn Gln Gly Ser

35

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<213> Insertion peptide

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Leu Gln Ala Gly Leu Cys Gly Ser

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33

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Ser Glu Gln Lys Gln Leu Gln Lys Arg Phe Gly Gly Phe Thr Gly Gly

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